Amendments to the Specification:

Please insert the Sequence Listing being filed concurrently herewith into the specification.

Please replace paragraph 133 with the following.

For example, a duplex comprising an antisense strand having the sequence CGAGAGGCGGACGGGACCG [SEQ ID No. 161] and having a two-nucleobase overhang of deoxythymidine(dT) would have the following structure:

```
cgagaggcggacgggaccgTT  Antisense Strand [SEQ ID No. 162]
||||||||||||||||||
TTgctctccgcctgccctggc   Complement [SEQ ID No. 163]
```

Please replace paragraph 134 with the following.

In another embodiment, a duplex comprising an antisense strand having the same sequence CGAGAGGCGGACGGGACCG may be prepared with blunt ends (no single stranded overhang) as shown:

```
cgagaggcggacgggaccg   Antisense Strand [SEQ ID No. 161]
||||||||||||||||||
gctctccgcctgccctggc   Complement [SEQ ID No. 164]
```

Please replace paragraph 142 with the following.

In accordance with the present invention, a series of antisense sequences were designed to target different regions of the human CD40 mRNA, using published sequences [Stamenkovic et al., *EMBO J.*, *8*, 1403 (1989); GenBank accession number X60592, SEQ ID No. 85]. The sequences are shown in Table 1.

Please amend Table 4, spanning pages 83-87 as follows.

Table 4
CD40 Antisense Sequence Alignment

SEQ ID NO:

	1 15	16 30	31 45	46 60	61 75	76 90
[9] 173	----------	----------	----------	----------	----------	----------TGC
[8] 172	----------	----------	----------	----------	----------	--------TGCTTGC
[7] 171	----------	----------	----------	----------	----------	--TGGGGCTGCTTGC
[6] 170	----------	----------	----------	----------	----------TCC	TCTGGGGCTGCTTGC
[5] 169	----------	----------	----------	---TGGTTCGTCTGC	CTCTGC---------	----------
[4] 168	----------	----------	----------	--ATGGTTCGTCTGC	CTCTG----------	----------
[3] 167	----------	----------TGCCG	CCTGGTCTCACCT--	----------	----------	----------
[2] 166	----------	----TGGTCCTGCCG	CCTGGTC--------	----------	----------	----------
[1] 165	----------	--AGTGGTCCTGCCG	CCTGG----------	----------	----------	----------
X60592-CD40	GCCTCGCTCGGGCGC	CCAGTGGTCCTGCCG	CCTGGTCTCACCTCG	CCATGGTTCGTCTGC	CTCTGCAGTGCGTCC	TCTGGGGCTGCTTGC

	91 105	106 120	121 135	136 150	151 165	166 180
[19] 183	----------	----------	----------	----------	----------	----------AC
[18] 182	----------	----------	----------	----------	----------	----------AGGAC
[17] 181	----------	----------	----------	----------	----------T	TGTGCCAGCCAGGAC
[16] 180	----------	----------	----------	----------	----------TCTT	TGTGCCAGCCAGGA-
[15] 179	----------	----------	----------	----------	-----TGCTGTTCTT	TGTGCCAG-------
[14] 178	----------	----------	----------	----------	-TCAGTGCTGTTCTT	TGTG----------
[13] 177	----------TC	CAGAACCACCCACTG	C----------	----------	----------	----------
[12] 176	----------CCATC	CAGAACCACCCAC--	----------	----------	----------	----------
[11] 175	-------TGTCCATC	CAGAACCACC-----	----------	----------	----------	----------
[10] 174	-GACCGCTGTCCATC	CAGA----------	----------	----------	----------	----------
[9] 173	TGACCGCTGTCCATC	----------	----------	----------	----------	----------
[8] 172	TGACCGCTGTC----	----------	----------	----------	----------	----------
[7] 171	TGACC----------	----------	----------	----------	----------	----------
X60592-CD40	TGACCGCTGTCCATC	CAGAACCACCCACTG	CATGCAGAGAAAAAC	AGTACCTAATAAACA	GTCAGTGCTGTTCTT	TGTGCCAGCCAGGAC

Table 4, continued

```
                181         195 196         210 211         225 226         240 241         255 256         270
[27] 191        --------------- --------------- --------------- --------------- --------------- -----------GAGA
[26] 190        --------------- --------------- --------------- --------------- ---------TAGACA CCTGGAACAGAG---
[25] 189        --------------- --------------- -----------TGCC TTCCTTGCGGTGAA- --------------- ---------------
[24] 188        --------------- --------------- CTGAAACGGAATGCC TTC------------ --------------- ---------------
[23] 187        --------------- ---------AGTTCA CTGAAACGGAAT--- --------------- --------------- ---------------
[22] 186        --------------- ACTGCACAGAGTTCA CTG------------ --------------- --------------- ---------------
[21] 185        ---------TGAGTG ACTGCACAGAGT--- --------------- --------------- --------------- ---------------
[20] 184        ----ACTGGTGAGTG ACTGCAC-------- --------------- --------------- --------------- ---------------
[19] 183        AGAAACTGGTGAGTG A--------------- --------------- --------------- --------------- ---------------
[18] 182        AGAAACTGGTGAG-- --------------- --------------- --------------- --------------- ---------------
[17] 181        AG------------- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     AGAAACTGGTGAGTG ACTGCACAGAGTTCA CTGAAACGGAATGCC TTCCTTGCGGTGAAA GCGAATTCCTAGACA CCTGGAACAGAGAGA

                271         285 286         300 301         315 316         330 331         345 346         360
[37] 201        --------------- --------------- --------------- --------------- --------------- ---------------T
[36] 200        --------------- --------------- --------------- --------------- --------------- --ACCATCTGCACCT
[35] 199        --------------- --------------- --------------- --------------- --------------G ACACCATCTGCACCT
[34] 198        --------------- --------------- --------------- --------------- ---CCTCAGAAACAG ACACCA---------
[33] 197        --------------- --------------- --------------- --------------- -CACCTCAGAAACAG ACAC-----------
[32] 196        --------------- --------------- --------------- ------AGCAGAAGG GCACCTCAG------ ---------------
[31] 195        --------------- --------------- --------------- --GTCCAGCAGAAGG GCACC---------- ---------------
[30] 194        --------------- ------ACTGCGACC CCAACCTAG------ --------------- --------------- ---------------
[29] 193        --------------- ---AATACTGCGACC CCAACC--------- --------------- --------------- ---------------
[28] 192        --------------- ACAAATACTGCGACC CCA------------ --------------- --------------- ---------------
[27] 191        CACACTGCCACCAG- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     CACACTGCCACCAGC ACAAATACTGCGACC CCAACCTAGGGCTTC GGGTCCAGCAGAAGG GCACCTCAGAAACAG ACACCATCTGCACCT
```

Table 4, continued

```
                361         375 376         390 391         405 406         420 421         435 436         450
[44] 208        --------------- --------------- --------------- --------------- --------------- ----------GATTG
[43] 207        --------------- --------------- --------------- --------------- -----------TTTG GGGTCAAGCAGATT-
[42] 206        --------------- --------------- --------------- ----------CTCAT GCTCGCCCGGCTT-- ---------------
[41] 205        --------------- --------------- ----------CTGTG TCCTGCACCGCTC-- --------------- ---------------
[40] 204        --------------- --------------- ----TGAGAGCTGTG TCCTGCA-------- --------------- ---------------
[39] 203        --------------- --------------- CCTGTGAGAGCTGTG TCC------------ --------------- ---------------
[38] 202        ---AAGAAGGCTGGC ACTGTA--------- --------------- --------------- --------------- ---------------
[37] 201        GTGAAGAAGGCTGGC AC------------- --------------- --------------- --------------- ---------------
[36] 200        GTGAA---------- --------------- --------------- --------------- --------------- ---------------
[35] 199        GT------------- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     GTGAAGAAGGCTGGC ACTGTACGAGTGAGG CCTGTGAGAGCTGTG TCCTGCACCGCTCAT GCTCGCCCGGCTTTG GGGTCAAGCAGATTG

                451         465 466         480 481         495 496         510 511         525 526         540
[56] 220        --------------- --------------- --------------- --------------- --------------- -------------GA
[55] 219        --------------- --------------- --------------- --------------- --------------- ------ACCCTTGGA
[54] 218        --------------- --------------- --------------- --------------- ------------AA AATGTCACCCTTGGA
[53] 217        --------------- --------------- --------------- ----------TGTGT CATCTGCTTTCGA-- ---------------
[52] 216        --------------- --------------- --------------- ----CTCCAATGTGT CATCTGC-------- ---------------
[51] 215        --------------- --------------- --------------- -CTTCTCCAATGTGT CATC----------- ---------------
[50] 214        --------------- --------------- ---------TCGGCT TCTTCTCCAATG--- --------------- ---------------
[49] 213        --------------- --------TGCGAGC CCTGCCCAGTC---- --------------- --------------- ---------------
[48] 212        --------------- -----ATCTGCGAGC CCTGCCCA------- --------------- --------------- ---------------
[47] 211        --------------- --ACCATCTGCGAGC CCTGC---------- --------------- --------------- ---------------
[46] 210        ------------CTG ATACCATCTGCGAGC --------------- --------------- --------------- ---------------
[45] 209        -TACAGGGGTTTCTG ATAC----------- --------------- --------------- --------------- ---------------
[44] 208        CTACAGGGGTTTC-- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     CTACAGGGGTTTCTG ATACCATCTGCGAGC CCTGCCCAGTCGGCT TCTTCTCCAATGTGT CATCTGCTTTCGAAA AATGTCACCCTTGGA
```

Table 4, continued

```
                541         555 556         570 571         585 586         600 601         615 616         630
[65] 229        --------------- --------------- --------------- --------------- --------------- ----------AGCCC
[64] 228        --------------- --------------- --------------- --------------- --------------- -----CTGAGAGCCC
[63] 227        --------------- --------------- --------------- --------------- ------GTCCCCAGG ATCGGCTGA------
[62] 226        --------------- --------------- --------------- -----------GTTG TCTGTGGTCCCCAG- ---------------
[61] 225        --------------- --------------- --------------- ----GACTGATGTTG TCTGTGG-------- ---------------
[60] 224        --------------- --------------- ----GGCAGGCACAA ACAAGAC-------- --------------- ---------------
[59] 223        --------------- -------------C AACAGGCAGGCACAA AC-------------- --------------- ---------------
[58] 222        --------------- --GACCTGGTTGTGC AACAG---------- --------------- --------------- ---------------
[57] 221        -----TGTGAGACCA AAGACCTG------- --------------- --------------- --------------- ---------------
[56] 220        CAAGCTGTGAGACCA A-------------- --------------- --------------- --------------- ---------------
[55] 219        CAAGCTGTG------ --------------- --------------- --------------- --------------- ---------------
[54] 218        C--------------- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     CAAGCTGTGAGACCA AAGACCTGGTTGTGC AACAGGCAGGCACAA ACAAGACTGATGTTG TCTGTGGTCCCCAGG ATCGGCTGAGAGCCC

                631         645 646         660 661         675 676         690 691         705 706         720
[69] 233        --------------- --------------- --------------- --------------- ------------CCA AGAAGCCAACCAATA
[68] 232        --------------- --------------- --------------- ---TGCTGGTCTTTA TCAAAA--------- ---------------
[67] 231        --------------- --------------- -------CATCCTCT TGGTGCTGGT----- --------------- ---------------
[66] 230        --------------- -----------ATCC TGTTTGCCATCCTC- --------------- --------------- ---------------
[65] 229        TGGTGGTGATCCC-- --------------- --------------- --------------- --------------- ---------------
[64] 228        TGGTGGTG------- --------------- --------------- --------------- --------------- ---------------
X60592-CD40     TGGTGGTGATCCCCA TCATCTTCGGGATCC TGTTTGCCATCCTCT TGGTGCTGGTCTTTA TCAAAAAGGTGGCCA AGAAGCCAACCAATA
```

Table 4, continued

```
                721         735 736         750 751         765 766         780 781         795 796         810
[78] 242        --------------- --------------- --------------- --------------- --------------- --------------T
[77] 241        --------------- --------------- --------------- --------------- --------------- ----------GACTT
[76] 240        --------------- --------------- --------------- --------------- --------------- CAGTGCAGGAGACTT
[75] 239        --------------- --------------- --------------- --------------T CCAACACTGCTGCTC CA-------------
[74] 238        --------------- --------------- --------------- ACGATCTTCCTGGCT CCA------------ ---------------
[73] 237        --------------- --------------- --------------G ACGATCTTCCTGGCT CC------------- ---------------
[72] 236        --------------- --------------- ---TCAATTTTCCCG ACGATC--------- --------------- ---------------
[71] 235        --------------- --------------G AGATCAATTTTCCCG AC------------- --------------- ---------------
[70] 234        --------CACCCCA AGCAGGAACCC---- --------------- --------------- --------------- ---------------
X60592-CD40     AGGCCCCCCACCCCA AGCAGGAACCCCAGG AGATCAATTTTCCCG ACGATCTTCCTGGCT CCAACACTGCTGCTC CAGTGCAGGAGACTT

                811         825 826         840 841         855 856         870 871         885 886         900
[81] 245        --------------- --------------- --------------- --------------- --AGACAGTGAGGCT GCACC----------
[80] 244        --------------- --------------- --------------- -----TCAGTGCAGG AGAGACAG------- ---------------
[79] 243        --------------- --------CAGGAGG ATGGCAAAGAG---- --------------- --------------- ---------------
[78] 242        TACATGGATGCCAAC CG------------- --------------- --------------- --------------- ---------------
[77] 241        TACATGGATGCCA-- --------------- --------------- --------------- --------------- ---------------
[86] 240        TAC------------ --------------- --------------- --------------- --------------- ---------------
X60592-CD40     TACATGGATGCCAAC CGGTCACCCAGGAGG ATGGCAAAGAGAGTC GCATCTCAGTGCAGG AGAGACAGTGAGGCT GCACCCACCCAGGAG

                901         915 916         930 931         945 946         960 961         975 976         990
[84] 248        --------------- --------------- --------------- --------------- --------------- GAGCTATGCCCAGTC
[83] 247        --------------- --------------- --------------- --------CAGGGGT GCAGGCAGAAG---- ---------------
[82] 246        ---------GTGGGC AAACAGGCAGTT--- --------------- --------------- --------------- ---------------
X60592-CD40     TGTGGCCACGTGGGC AAACAGGCAGTTGGC CAGAGAGCCTGGTGC TGCTGCTGCAGGGGT GCAGGCAGAAGCGGG GAGCTATGCCCAGTC

                991       1004
[84] 248        AGT-----------
X60592-CD40     AGTGCCAGCCCCTC
```

Please replace paragraph 192 with the following.

Total RNA was isolated using an RNeasy Mini Kit (Qiagen). Two-step RT-PCR was performed using primers complementary to sequences of the CD40 gene (Genbank accession# M83312, incorporated herein as SEQ ID NO: 92). Reverse transcription was performed using a reverse primer (5'-TGATATAGAGAAACACCCCGAAAATGG-3'; SEQ ID NO: 93) complementary to sequence in exon 7. The resulting cDNA was subjected to 35 cycles of PCR using a forward primer consisting of a sequence span identical to that found in exon 5 of the gene (5'-GCCACTGAGACCACTGATACCGTCTGT-3'; SEQ ID NO: 94) as well as the reverse primer used for cDNA generation. The resulting PCR products were separated on a 1.6% agarose gel. PCR products were excised and the DNA purified. The resulting products were sequenced using primers used in PCR. Real-time quantitative RT-PCR was performed on total RNA from BCL_1 or primary macrophages using an ABI Prism® 7700. Primer and dual labeled probe sequences were as follows:

Mouse IL-12 p40:

forward 5'-GCCAGTACACCTGCCACAAA- 3', SEQ ID No. 95
reverse 5'-GACCAAATTCCATTTTCCTTCTTG-3', SEQ ID No. 96
probe 5'-FAM-AGGCGAGACTCTGAGCCACTCACATCTG-TAMRA-3', SEQ ID No. 97

Mouse CD18:

Forward 5'-CTGCATGTCCGGAGGAAATT-3' SEQ ID No. 98
Reverse 5'-AGCCATCGTCTGTGGCAAA-3' SEQ ID No. [9] 99

Probe 5′-FAM-CTGGCGCAATGTCACGAGGCTG-TAMRA-3′, SEQ ID No. 100

Mouse CD40, Type 1:

Forward 5′-CACTGATACCGTCTGTCATCCCT-3′ SEQ ID No. 101

Reverse 5′-AGTTCTTATCCTCACAGCTTGTCCA-3′ SEQ ID No. 102

Probe 5′-FAM-AGTCGGCTTCTTCTCCAATCAGTCATCACTT-TAMRA-3′ SEQ ID No. 103

Mouse CD40, Type 2:

Forward 5′-CACTGATACCGTCTGTCATCCCT-3′ SEQ ID No. 104

Reverse 5′-CCACATCCGGGACTTTAAACCTTGT-3′ SEQ ID No. 105

Probe 5′-FAM-CCAGTCGGCTTCTTCTCCAATCAGTCA-TAMRA-3′ SEQ ID No. 106

Mouse CD40:

Forward 5′-TGTGTTACGTGCAGTGACAAACAG-3′ SEQ ID No. 107

Reverse 5′-GCTTCCTGGCTGGCACAA-3′ SEQ ID No. 108

Probe 5′-FAM-CCTCCACGATCGCCAGTGCTGTG-TAMRA-3′ SEQ ID No. 109

Mouse cyclophilin:

Forward 5′-TCGCCGCTTGCTGCA-3′ SEQ ID No. 110

Reverse 5′-ATCGGCCGTGATGTCGA-3′ SEQ ID No. 111

Probe 5′-FAM-CCATGGTCAACCCCACCGTGTTC-TAMRA-3′ SEQ ID No. 112

Please amend Table 9, spanning pages 112-121 with the following.

Table 9

Additional PNA Cationic Conjugate Compounds of SEQ ID NO: 124

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
208529-1		K		80, 98, 100	stable	stable
278640-1	K	K		80	*n.d.*	
278641-1	K_2	K		90	*n.d.*	
278642-1	K_3	K		80	*n.d.*	
278643-1	K_4 ~~(SEQ ID NO: 161)~~	K		100	*n.d.*	
278644-1	K_5 ~~(SEQ ID NO: 162)~~	K		70	*n.d.*	
278645-1	K_6 ~~(SEQ ID NO: 163)~~	K		50	*n.d.*	
278646-1	K_7 ~~(SEQ ID NO: 164)~~	K		30	*n.d.*	
278647-1	K_8 ~~(SEQ ID NO: 165)~~	K		20, 30, 35, 30, 15	5.7	1.4
287294-1	K_8	K	4 mm	100	*n.d.*	
287293-1	K_6	K	4 mm	100	*n.d.*	
284381-1		K_2		95	*n.d.*	
279866-1		K_4		85	6.5	1.6
284375-1		K_8		40, 35, 35, 40, 35, 45, 73, 68	1	0.25
290075-1	R	K		100	*n.d.*	
290076-1	R_2	K		90	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
290077-1	R_3	K		90	*n.d.*	
290078-1	R_4 ~~(SEQ ID NO: 166)~~	K		80	*n.d.*	
290079-1	R_5 ~~(SEQ ID NO: 167)~~	K		80	*n.d.*	
297780-1	R_6 ~~(SEQ ID NO: 168)~~	K		75	*n.d.*	
290081-1	R_7 ~~(SEQ ID NO: 169)~~	K		70	*n.d.*	
290082-2	R_8 ~~(SEQ ID NO: 170)~~	K		60	3.2	0.8
301010-1	D-R_8	K		49	*n.d.*	
299870-1		K_5RK_2 (SEQ ID NO: 171)		48	*n.d.*	
299871-1		D(K_5RK_2) (SEQ ID NO: 172)		53	*n.d.*	
284382-1	K_2	K_2		85	*n.d.*	
279867-1	K_4	K_4		75	*n.d.*	
284383-1	Ada-O	K_2		80	*n.d.*	
284384-1	Ada-O-K_2	K_2		85	*n.d.*	
279975-1	Ada-O	K_4		95	*n.d.*	
279976-1	Ada-O-K_4	K_4		75	*n.d.*	
284376-1	Ada-O	K_8		40	*n.d.*	
284385-1	Pam-O	K_2		n/a tox.	*n.d.*	
284386-1	Pam-O-K_2	K_2		n/a tox.	*n.d.*	
283582-1	Pam-O	K_4		70	*n.d.*	
283583-1	Pam-O-K_4	K_4		60	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
284377-1	Pam-O	K_8		n/a tox.	*n.d.*	
290061-1	Ibu-O	K_2		80	*n.d.*	
287086-1	Ibu-O	K_8		30	1	0.25
311573-1	Ibu-O-K_8	K		n.d.	*n.d.*	
290063-1	CHA-O	K_2		95	*n.d.*	
290064-1	Chol-O-	K_2		n/a tox.	*n.d.*	
292097-1	CHA-O-K_8	K		55	*n.d.*	
292098-1	Chol-O-K_8	K		n/a tox.	*n.d.*	
298110-1	Branch1-K	K		60	*n.d.*	
298111-1	Branch3-K	K		85	*n.d.*	
298112-1	Branch4-K	K		60	*n.d.*	
298113-1	Branch5-K	K		75	*n.d.*	
298114-1	Branch6-K	K		70	*n.d.*	
298116-1	Branch2-K	K		40	*n.d.*	
303537-1	RacaRRacaRRacaRR	K		23, 29	2	0.5
303540-1	KacaKKacaKKacaKK	K		70	*n.d.*	
303538-1	RacaRacaRacaRacaRacaRacaR	K		40	*n.d.*	
309743-1	dR.aca.dR.dR.aca.dR.dR.aca.dR.dR	K		35	*n.d.*	
303539-1	KacaKacaKacaKacaKacaKacaK	K		61	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
291341-1	KGKKGKGK ~~(SEQ ID NO: 173)~~	K		87	*n.d.*	
291342-1	KaocKKaocKaocK	K		79	*n.d.*	
330890-1	hR-O-hR-hR-O-hR-hR-O-hR-hR	K		25 at 3 uM	59	12
338896-1	hR-O-R-hR-O-R-hR-O-R-hR	K		49	2	0.5
338897-1	R-O-hR-R-O-hR-R-O-hR-R	K		54	4	1
315570-1	RacaRRacaRRacaRR-PKKKRKV	K		25	*n.d.*	
315571-1	RacaRRacaRRacaRR-KKVKPKR	K		41	*n.d.*	
315650-1	PKKKRKV-RacaRRacaRRacaRR	K		44	*n.d.*	
315573-1	KKVKPKR-RacaRRacaRRacaRR	K		31	*n.d.*	
309860-1	R-βA-RR-βA-RRβA-RR	K		27	*n.d.*	
309883-1	R-abu-RR-abu-RR-abu-RR	K		26	*n.d.*	
309861-1	R-aoc-RR-aoc-RR-aoc-RR	K		25	*n.d.*	
309864-1	R-aca-RR-aca-RR-aca-RR-aca	K		20	*n.d.*	
309862-1	R-O-RR-O-RR-O-RR	K		24	2	0.5

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
309865-1	RR-aca-RR-aca-RR	K		40	*n.d.*	
309866-1	R-aca-RR-aca-RR	K		58	*n.d.*	
309884-1	R-inp-RR-inp-RR-inp-RR	K		29	*n.d.*	
309885-1	R-amc-RR-amc-RR-amc-RR	K		27	*n.d.*	
291350-2	$(ßK)_8$	K		66	*n.d.*	
309843-1	ßK-ßK-KKKK-ßK-ßK	K		52	*n.d.*	
309844-1	$(K\text{-}ßK)_4$	K		62	*n.d.*	
309845-1	KK-ßK-KK-ßK-KK	K		61	*n.d.*	
303536-1	$D\text{-}(Orn)_8$	K		67	*n.d.*	
303327-1		$(Orn)_8$		64	*n.d.*	
301011-2	$(Orn)_8$	K		77	> 48	> 12
309143-1	Orn-Orn-KKKK-Orn-Orn	K		52	*n.d.*	
309144-1	$(K\text{-}Orn)_4$	K		42	*n.d.*	
309145-1	KK-Orn-KK-Orn-KK	K		34	19	4.75
311069-1	KKKKK-Orn-KK	K		50	*n.d.*	
311070-1	KK-Orn-KKKKK	K		53	*n.d.*	
287292-2	$(dK)_8$	K		54	stable	> 48
305390-1	dKdK-KKKK-dKdK	K		60	*n.d.*	
305391-1	K-dK-K-dK-K-dK-K-dK	K		69	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
305392-1	KK-dK-KK-dK-KK	K		62	stable	> 48
311071-1	KKKKK-dK-KK	K		61	*n.d.*	
311072-1	KK-dK-KKKKK	K		59	*n.d.*	
305393-1	RRKKKKKRR ~~(SEQ ID NO: 174)~~	K		65	*n.d.*	
305394-1	KRKRKRKR ~~(SEQ ID NO: 175)~~	K		52	*n.d.*	
305395-1	KKRKKRKK ~~(SEQ ID NO:176)~~	K		43	2.5	0.6
308579-1	$(hK)_8$	K		31	18	4.5
308580-1	hKhK-KKKK-hKhK	K		34	*n.d.*	
308581-1	K-hK-K-hK-K-hK-K-hK	K		32	*n.d.*	
308582-1	KK-hK-KK-hK-KK	K		31	7.5	1.9
316409-1	$(Dab)_8$	K		77	> 48	> 12
316410-1	$(Dab)_2$-K-$(Dab)_2$ -K-$(Dab)_2$	K		64	*n.d.*	
316411-1	$(Dab\text{-}K)_4$	K		52	*n.d.*	
316412-1	KK-Dab-KK-Dab-KK	K		38	40	10
316427-1	$(K\text{-}ab)_8$	K		47	*n.d.*	
316428-1	$(K\text{-}(K\text{-}ab))_4$	K		41	*n.d.*	
316429-1	KK-(K-ab)-KK-(K-ab)-KK	K		39	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
316430-1	$(K\text{-}ab)_2$-K-$(K\text{-}ab)_2$-K-$(K\text{-}ab)_2$	K		55	*n.d.*	
325598-1	$(dmK)_8$	K		71	stable	
325599-1	$(K\text{-}dmK)_4$	K		53	*n.d.*	
325600-1	KK-dmK-KK-dmK-KK	K		41	23	5.8
325601-1	$(dmK)_2$-K-$(dmK)_2$-K-$(dmK)_2$	K		63	*n.d.*	
326744-1	$(hR)_8$	K		30, 20	15.4	3.9
	$(hhR)_8$	K		n/a	stable	stable
333677-1	$(K\text{-}hR)_4$	K		44	*n.d.*	
333678-1	KK-hR-KK-hR-KK	K		36	*n.d.*	
338894-1	$(DhR)_8$	K		n/a tox.	*n.d.*	
338895-1	RR-DhR-RR-DhR-RR	K		67	23.6	5.9
326746-1	$(norR)_8$	K		90 at 3 uM	> 48	> 12
333674-1	$G(pK)_8$	K		56	> 48	> 12
333675-1	$(K\text{-}pK)_4$	K		70	*n.d.*	
333676-1	KK-pK-KK-pK-KK	K		60	29	7.25
332593-1	$(H)_8$ ~~(SEQ ID NO: 177)~~	K		64	44.5	11
332672-1	$(KH)_4$ ~~(SEQ ID NO:178)~~	K		73	*n.d.*	
332673-1	KKHKKHKK ~~(SEQ ID NO: 179)~~	K		52	5.7	1.4
332674-1	KKGKKGKK ~~(SEQ ID~~	K		59	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
	~~NO: 180)~~					
313685-1	K_7-Ci	K		65	*n.d.*	
313686-1	K_6-Ci-K	K		59	*n.d.*	
313687-1	K_5-Ci-K_2	K		53	*n.d.*	
313688-1	K_4-Ci-K_3	K		52	*n.d.*	
313689-1	K_3-C-K_4	K		57	*n.d.*	
313690-1	K_2-Ci-K_5	K		55	*n.d.*	
313691-1	K-Ci-K_6	K		57	*n.d.*	
313692-1	Ci-K_7	K		52	*n.d.*	
313693-1	KK-Ci-KK-Ci-KK	K		65, 67	*n.d.*	
310755-1	K_8–βA	K		43	*n.d.*	
310756-1	K_8–aca	K		48	*n.d.*	
310757-1	K_8–aoc	K		54	*n.d.*	
310758-1	K_8–adc	K		68	*n.d.*	
291335-2	K_8–aoc-aoc	K		62	*n.d.*	
310753-1	K_8–O	K		44	*n.d.*	
310754-1	K_8–O-O	K		46	*n.d.*	
330775-1	$(dK)_8$-FRGO	K		46	2.8	0.7
330776-1	$(dK)_8$-dF-dRGO	K		54	*n.d.*	
330777-1	$(dK)_8$-ALALGO	K		37	8.7	2.2
330778-1	$(dK)_8$-dA-dLdAdLGO	K		36	*n.d.*	

Isis #-Lot#	N-terminal modification	C-terminal modification	notes	CD40 Protein (% UTC @ 10 μM)	$t_{1/2}$ [h] in 25% mouse serum	Est. $t_{1/2}$ [h] in 100% mouse serum
335296-1	$(dK)_8$-WEHDLO	K		59	> 48	. 12
335299-1	$(dK)_8$-dW-dE-dH-dD-dL-O	K		64	*n.d.*	
335297-1	$(dK)_8$-D-E-V-D-L-O	K		90	> 48	> 12
335300-1	$(dK)_8$-dD-dE-dV-dD-dL-O	K		89	*n.d.*	
330781-1	$(dK)_8$-G-F-L-G-O	K		38	> 48	> 12
330782-1	$(dK)_8$-G-dF-dL-G-O	K		39	*n.d.*	
339746-1	dK_8-Cys-disulfide-Cys-O	K		41	17	4.25
339747-1	dK_8-Cys-disulfide-Pen-O	K		35	30	7.5